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海洋巨大ウイルスとその宿主の多様性解析について

Diversity analysis of giant marine viruses and their hosts.

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研究成果概要

My research focuses around diversity analysis of megaviridae in sea water samples of Osaka and Uranouchi bay. Usually, the diversity analysis of megaviridae involves metagenomics[1]–[3], however recently a primer base method was published with promising results[4]. I have been improving the referenced method and generated datasets using the so called MEGAPRIMERs, a set of 82 primers which target the megaviridae polymerase B gene. The generated data is stored on the supercomputer. Additionally, I use the supercomputer to analyze MEGAPRIMER sequencing datasets using MAPS[4] and 18S rRNA sequencing data with qiime2[5] and I utilize python 3 and R scripts for data manipulation and plotting.

References

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